

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/674,311DATE: 08/26/96
TIME: 11:08:50

INPUT SET: SI2328.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: Olopade, Olufunmilayo I.

(ii) TITLE OF INVENTION: METHYLTHIOADENOSINE PHOSPHORYLASE
COMPOSITIONS AND METHODS OF USE IN
THE DIAGNOSIS AND TREATMENT OF
PROLIFERATIVE DISORDERS

(iii) NUMBER OF SEQUENCES: 15

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Arnold, White & Durkee
- (B) STREET: P.O. Box 4433
- (C) CITY: Houston
- (D) STATE: Texas
- (E) COUNTRY: United States of America
- (F) ZIP: 77210

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US Unknown
- (B) FILING DATE: Concurrently Herewith
- (C) CLASSIFICATION: Unknown

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 60/000,831
- (B) FILING DATE: 02-JUL-1995
- (C) CLASSIFICATION: Unknown

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Kitchell, Barbara S.
- (B) REGISTRATION NUMBER: 33,928
- (C) REFERENCE/DOCKET NUMBER: ARSB:509

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (512) 418-3000
- (B) TELEFAX: (512) 474-7577

RAW SEQUENCE LISTING PATENT APPLICATION US/08/674,311

DATE: 08/26/96
TIME: 11:08:53

INPUT SET: S12328.raw

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47
48 (2) INFORMATION FOR SEQ ID NO:1:
49
50 (i) SEQUENCE CHARACTERISTICS:
51 (A) LENGTH: 2269 base pairs
52 (B) TYPE: nucleic acid
53 (C) STRANDEDNESS: single
54 (D) TOPOLOGY: linear
55
56 (ix) FEATURE:
57 (A) NAME/KEY: CDS
58 (B) LOCATION: 122..970
59
60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
61
62 GAATTCCGCT CCGCACTGCT CACTCCCGCG CAGTGAGGTT GGCACAGCCA CCGCTCTGTG 60
63
64 GCTCGCTTGG TTCCCTTAGT CCCGAGCGCT CGCCCACTGC AGATTCCTTT CCCGTGCAGA 120
65
66 C ATG GCC TCT GGC ACC ACC ACC ACC GCC GTG AAG ATT GGA ATA ATT 166
67 Met Ala Ser Gly Thr Thr Thr Thr Ala Val Lys Ile Gly Ile Ile
68 1 5 10 15
69
70 GGT GGA ACA GGC CTG GAT GAT CCA GAA ATT TTA GAA GGA AGA ACT GAA 214
71 Gly Gly Thr Gly Leu Asp Asp Pro Glu Ile Leu Glu Gly Arg Thr Glu
72 20 25 30
73
74 AAA TAT GTG GAT ACT CCA TTT GGC AAG CCA TCT GAT GCC TTA ATT TTG 262
75 Lys Tyr Val Asp Thr Pro Phe Gly Lys Pro Ser Asp Ala Leu Ile Leu
76 35 40 45
77
78 GGG AAG ATA AAA AAT GTT GAT TGC ATC CTC CTT GCA AGG CAT GGA AGG 310
79 Gly Lys Ile Lys Asn Val Asp Cys Ile Leu Leu Ala Arg His Gly Arg
80 50 55 60
81
82 CAG CAC ACC ATC ATG CCT TCA AAG GTC AAC TAC CAG GCG AAC ATC TGG 358
83 Gln His Thr Ile Met Pro Ser Lys Val Asn Tyr Gln Ala Asn Ile Trp
84 65 70 75
85
86 GCT TTG AAG GAA GAG GGC TGT ACA CAT GTC ATA GTG ACC ACA GCT TGT 406
87 Ala Leu Lys Glu Glu Gly Cys Thr His Val Ile Val Thr Thr Ala Cys
88 80 85 90 95
89
90 GGC TCC TTG AGG GAG GAG ATT CAG CCC GGC GAT ATT GTC ATT ATT GAT 454
91 Gly Ser Leu Arg Glu Glu Ile Gln Pro Gly Asp Ile Val Ile Ile Asp
92 100 105 110
93
94 CAG TTC ATT GAC AGG ACC ACT ATG AGA CCT CAG TCC TTC TAT GAT GGA 502
95 Gln Phe Ile Asp Arg Thr Thr Met Arg Pro Gln Ser Phe Tyr Asp Gly
96 115 120 125
97
98 AGT CAT TCT TGT GCC AGA GGA GTG TGC CAT ATT CCA ATG GCT GAG CCG 550
99 Ser His Ser Cys Ala Arg Gly Val Cys His Ile Pro Met Ala Glu Pro

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100	130	135	140	
101				
102	TTT TGC CCC AAA ACG AGA GAG GTT CTT ATA GAG ACT GCT AAG AAG CTA			598
103	Phe Cys Pro Lys Thr Arg Glu Val Leu Ile Glu Thr Ala Lys Lys Leu			
104	145	150	155	
105				
106	GGA CTC CGG TGC CAC TCA AAG GGG ACA ATG GTC ACA ATC GAG GGA CCT			646
107	Gly Leu Arg Cys His Ser Lys Gly Thr Met Val Thr Ile Glu Gly Pro			
108	160	165	170	175
109				
110	CGT TTT AGC TCC CGG GCA GAA AGC TTC ATG TTC CGC ACC TGG GGG GCG			694
111	Arg Phe Ser Ser Arg Ala Glu Ser Phe Met Phe Arg Thr Trp Gly Ala			
112	180	185	190	
113				
114	GAT GTT ATC AAC ATG ACC ACA GTT CCA GAG GTG GTT CTT GCT AAG GAG			742
115	Asp Val Ile Asn Met Thr Thr Val Pro Glu Val Val Leu Ala Lys Glu			
116	195	200	205	
117				
118	GCT GGA ATT TGT TAC GCA AGT ATC GCC ATG GCG ACA GAT TAT GAC TGC			790
119	Ala Gly Ile Cys Tyr Ala Ser Ile Ala Met Ala Thr Asp Tyr Asp Cys			
120	210	215	220	
121				
122	TGG AAG GAG CAC GAG GAA GCA GTT TCG GTG GAC CGG GTC TTA AAG ACC			838
123	Trp Lys Glu His Glu Glu Ala Val Ser Val Asp Arg Val Leu Lys Thr			
124	225	230	235	
125				
126	CTG AAA GAA AAC GCT AAT AAA GCC AAA AGC TTA CTG CTC ACT ACC ATA			886
127	Leu Lys Glu Asn Ala Asn Lys Ala Lys Ser Leu Leu Leu Thr Thr Ile			
128	240	245	250	255
129				
130	CCT CAG ATA GGG TCC ACA GAA TGG TCA GAA ACC CTC CAT AAC CTG AAG			934
131	Pro Gln Ile Gly Ser Thr Glu Trp Ser Glu Thr Leu His Asn Leu Lys			
132	260	265	270	
133				
134	AAT ATG GCC CAG TTT TCT GTT TTA TTA CCA AGA CAT TAAAGTAGCA			980
135	Asn Met Ala Gln Phe Ser Val Leu Leu Pro Arg His			
136	275	280		
137				
138	TGGCTGCCCA GGAGAAAAGA AGACATTCTA ATTCCAGTCA TTTTGGAAT TCCTGCTTAA			1040
139				
140	CTTGAAAAAA ATATGGGAAA GACATGCAGC TTTCATGCCC TTGCCTATCA AAGAGTATGT			1100
141				
142	TGTAAGAAAG ACAAGACATT GTGTGTATTA GAGACTCCTG AATGATTTAG ACAACTTCAA			1160
143				
144	AATACAGAAG AAAAGCAAAT GACTAGTAAA CATGTGGGAA AAAATATTAC ATTTTAAGGG			1220
145				
146	GGAAAAAAA AACCACCA TTCTCTTCTC CCCCTATTAA ATTTGCAACA ATAAAGGGTG			1280
147				
148	GAGGGTAATC TCTACTTTCC TATACTGCCA AAGAATGTGA GGAAGAAATG GGAAGGGTG			1340
149				
150	GTTATTTATT GATGCGACTG TAAATTGGTA CAGTATTTCT GGAGGGCAAT TTGGTAAAAAT			1400
151				
152	GCATCAAAAG ACTTAAAAAT ACGGACGTCC TTTGGTGCTG GGAAGTCTAC ATCTAGCAAT			1460

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153
154 TTCTCTTTAA AACCATATCA GAGATGCATA CAAAGAATTA TATATAAAGA AGGGTGTTTA 1520
155
156 ATAATGATAG TTATAATAAT AAATAATTGA AACAATCTGA ATCCCTTGCA ATTGGAGGTA 1580
157
158 AATTATGTCT TAGTTATAAT CTAGATTGTG AATCAGCCAA CTGAAAATCC TTTTTCGATA 1640
159
160 TTTCAATGTC CTAAAAAGAC ACGGTTGCTC TATATATGAA GTGAAAAAAG GATATGGTAG 1700
161
162 CATTTTATAG TACTAGTTTT GCTTTAAAAT GCTATGTAAA TATACAAAAA AACTAGAAAAG 1760
163
164 AAATATATAT AACCTTGTTA TTGTATTTGG GGGAGGGATA CTGGGATAAT TTTTATTTTC 1820
165
166 TTTGAATCTT TCTGTGTCTT CACATTTTTC TACAGTGAAT ATAATCAAAT AGTAAAGGGC 1880
167
168 CGTAAAAATA AAAGTGGATT TAGAAAGATC CAGTTCTTGA AAACACTGTT TCTGGTAATG 1940
169
170 AAGCAGAATT TAAGTTGGTA ATATTAAGGT GAATGTCATT TAAGGGAGTT ACATCTTTAT 2000
171
172 TCTGCTAAAG AAGAGGATCA TTGATTTCTG TACAGTCAGA ACAGTACTTG GGTGTGCAAC 2060
173
174 AGCTTTCTGA GAAAAGCTAG GTGTATAATA GTTAACTGA AAGTTTAACT ATTTAAAAGA 2120
175
176 CTAAATGCAC ATTTTATGGT ATCTGATATT TTA AAAAGTA ATGTGAGCTT CTCCTTTTTA 2180
177
178 TGAGTTAAAT TATTTTATAC GAGTTGGTAA TTTGTGCCTT TTAATAAAGT GGAAGCTTGC 2240
179
180 TTTTAAAAA AAAAAAAAAA GCGGAATTC 2269
181
182

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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193
194 Met Ala Ser Gly Thr Thr Thr Thr Ala Val Lys Ile Gly Ile Ile Gly
195   1           5           10           15
196
197 Gly Thr Gly Leu Asp Asp Pro Glu Ile Leu Glu Gly Arg Thr Glu Lys
198           20           25           30
199
200 Tyr Val Asp Thr Pro Phe Gly Lys Pro Ser Asp Ala Leu Ile Leu Gly
201           35           40           45
202
203 Lys Ile Lys Asn Val Asp Cys Ile Leu Leu Ala Arg His Gly Arg Gln
204           50           55           60
205

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206 His Thr Ile Met Pro Ser Lys Val Asn Tyr Gln Ala Asn Ile Trp Ala
207 65 70 75 80
208
209 Leu Lys Glu Glu Gly Cys Thr His Val Ile Val Thr Thr Ala Cys Gly
210 85 90 95
211
212 Ser Leu Arg Glu Glu Ile Gln Pro Gly Asp Ile Val Ile Ile Asp Gln
213 100 105 110
214
215 Phe Ile Asp Arg Thr Thr Met Arg Pro Gln Ser Phe Tyr Asp Gly Ser
216 115 120 125
217
218 His Ser Cys Ala Arg Gly Val Cys His Ile Pro Met Ala Glu Pro Phe
219 130 135 140
220
221 Cys Pro Lys Thr Arg Glu Val Leu Ile Glu Thr Ala Lys Lys Leu Gly
222 145 150 155 160
223
224 Leu Arg Cys His Ser Lys Gly Thr Met Val Thr Ile Glu Gly Pro Arg
225 165 170 175
226
227 Phe Ser Ser Arg Ala Glu Ser Phe Met Phe Arg Thr Trp Gly Ala Asp
228 180 185 190
229
230 Val Ile Asn Met Thr Thr Val Pro Glu Val Val Leu Ala Lys Glu Ala
231 195 200 205
232
233 Gly Ile Cys Tyr Ala Ser Ile Ala Met Ala Thr Asp Tyr Asp Cys Trp
234 210 215 220
235
236 Lys Glu His Glu Glu Ala Val Ser Val Asp Arg Val Leu Lys Thr Leu
237 225 230 235 240
238
239 Lys Glu Asn Ala Asn Lys Ala Lys Ser Leu Leu Leu Thr Thr Ile Pro
240 245 250 255
241
242 Gln Ile Gly Ser Thr Glu Trp Ser Glu Thr Leu His Asn Leu Lys Asn
243 260 265 270
244
245 Met Ala Gln Phe Ser Val Leu Leu Pro Arg His
246 275 280
247
248
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/674,311

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INPUT SET: S12328.raw

Line	Error	Original Text
29	Wrong application Serial Number	(A) APPLICATION NUMBER: US Unknown
31	Wrong Classification	(C) CLASSIFICATION: Unknown
36	Wrong Classification	(C) CLASSIFICATION: Unknown